












## Summary

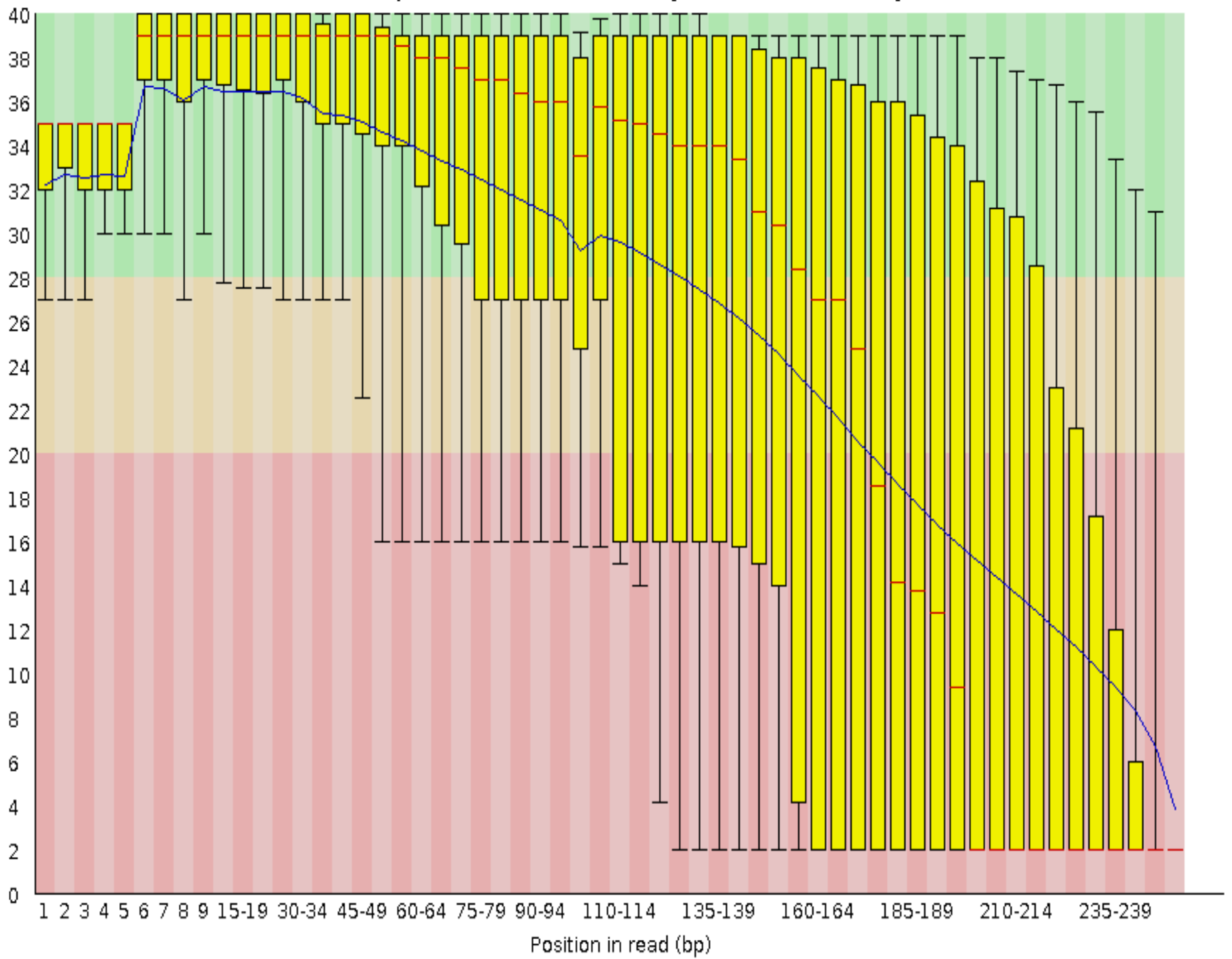
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## Basic Statistics

Measure	Value
Filename	BS-tag_seqprep_dupRemoved_ec_R2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	17663182
Sequences flagged as poor quality	0
Sequence length	250
%GC	43

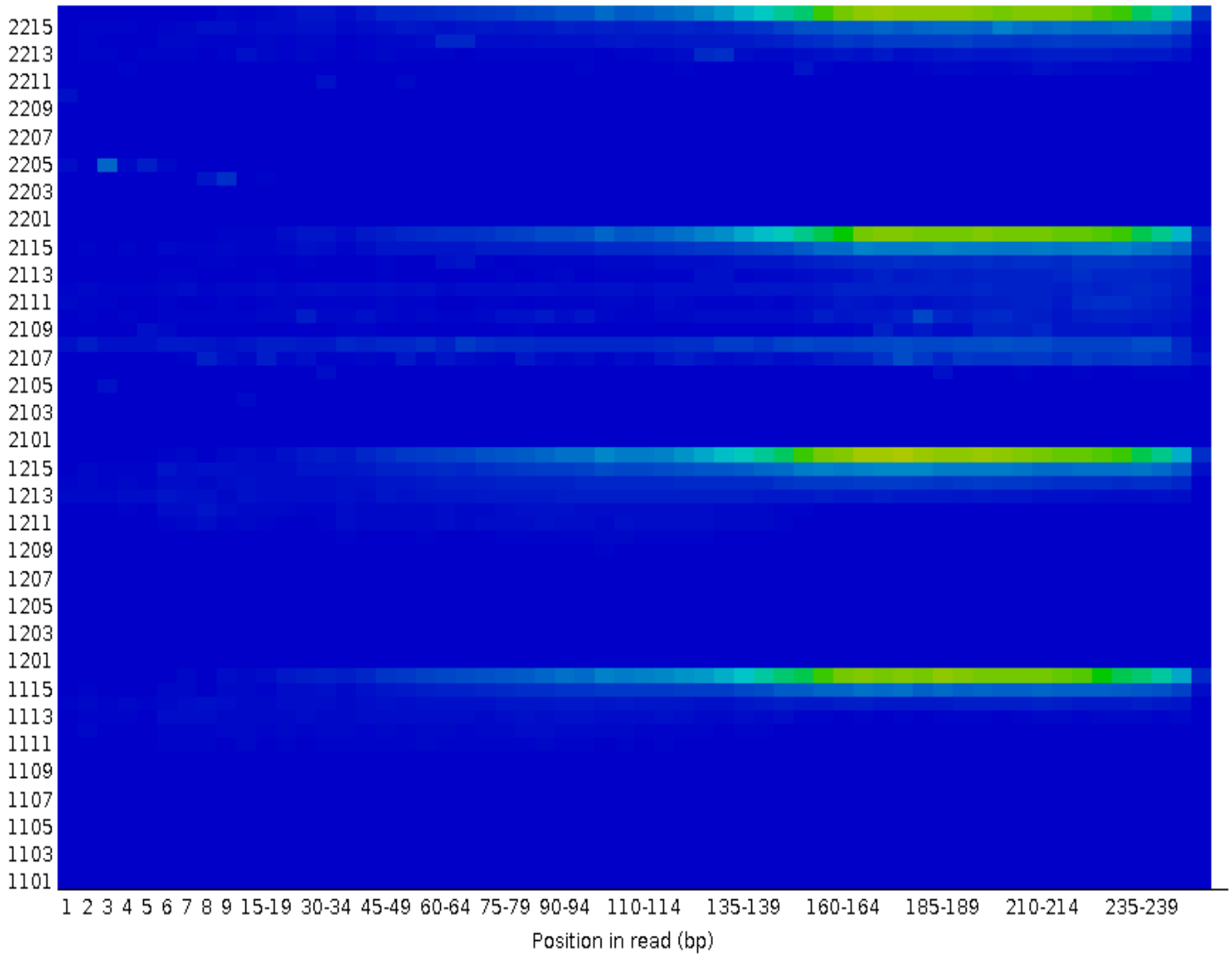
## Per base sequence quality

Quality scores across all bases (Sanger / Illumina 1.9 encoding)



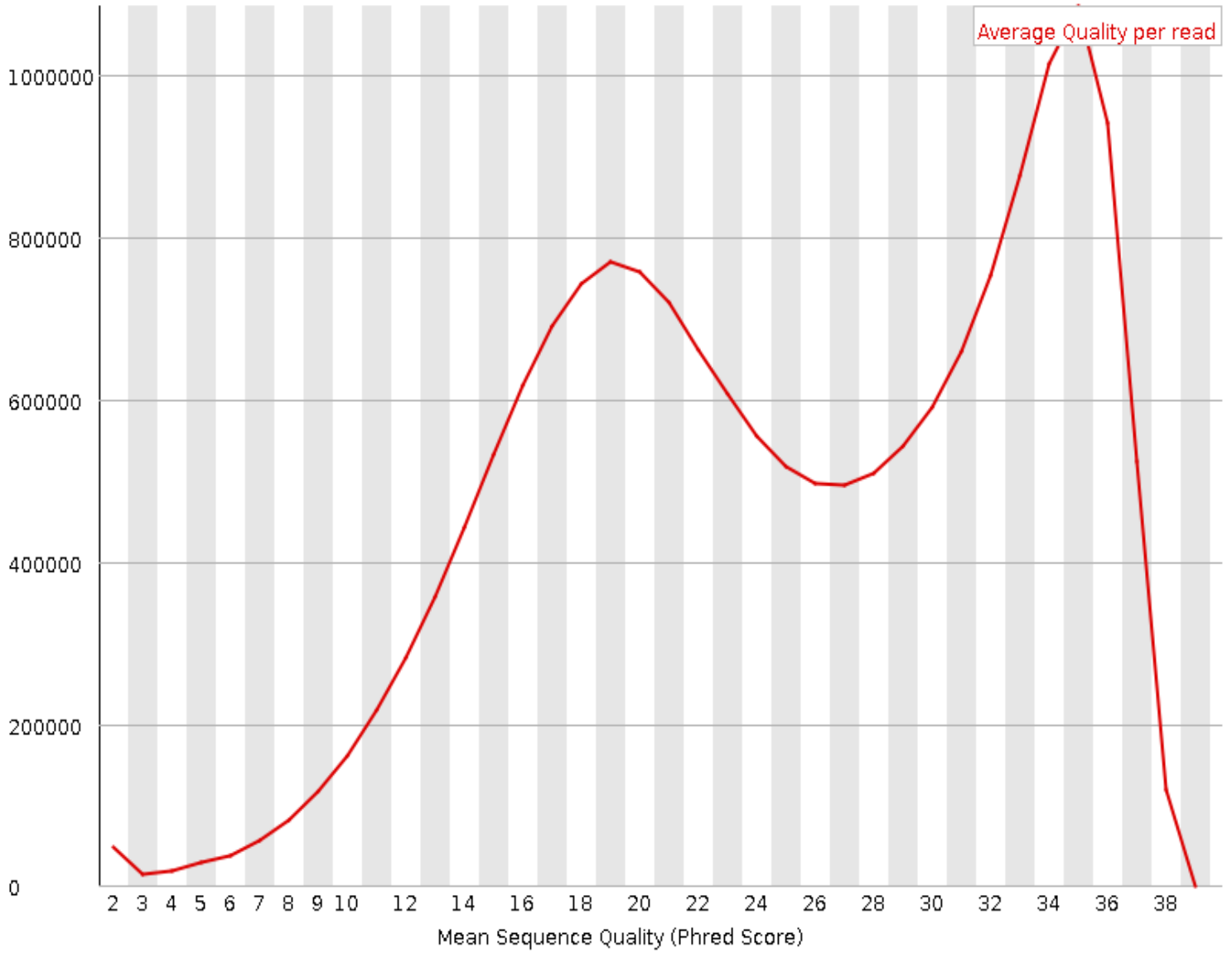
**! Per tile sequence quality**

Quality per tile



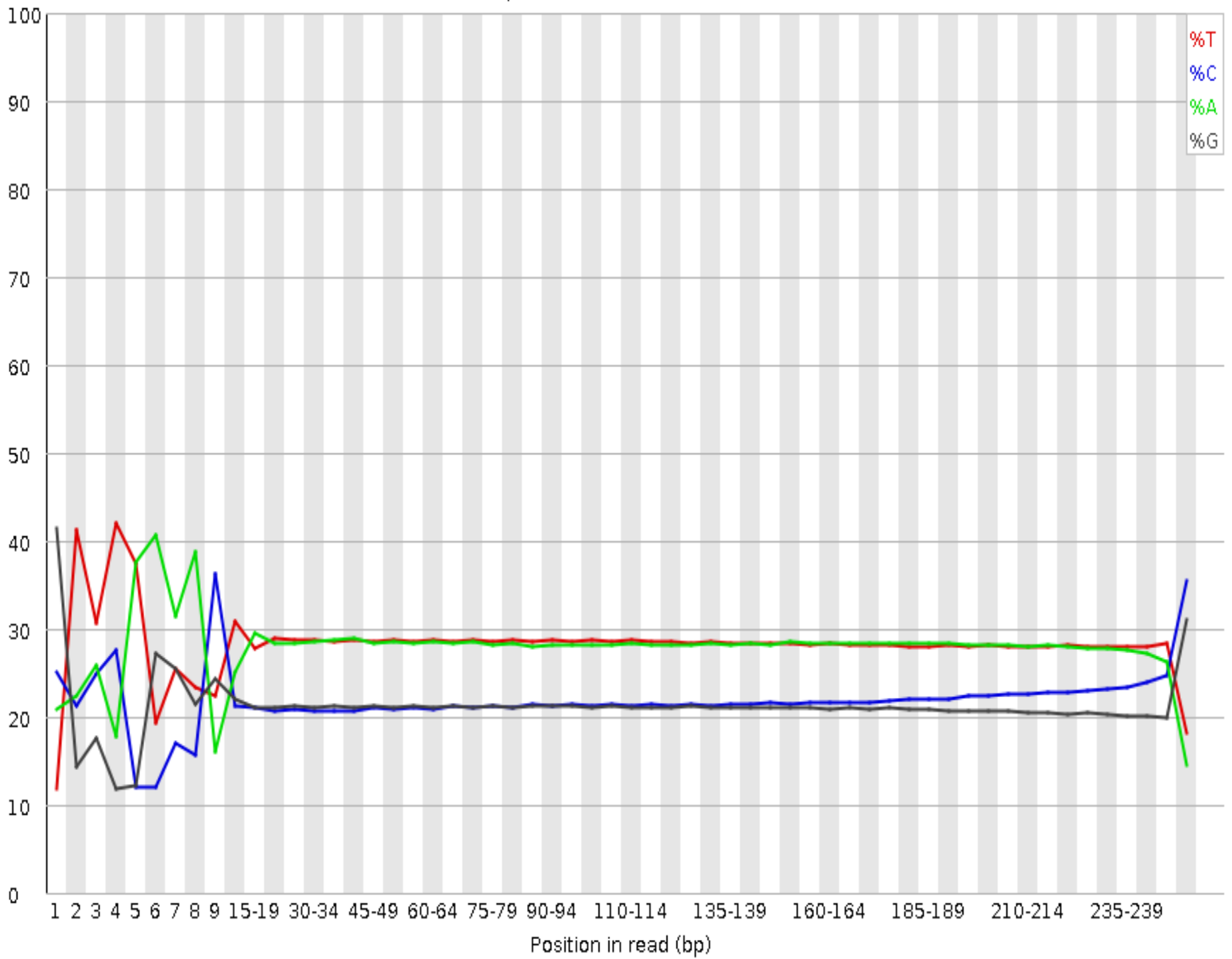
 **Per sequence quality scores**

Quality score distribution over all sequences

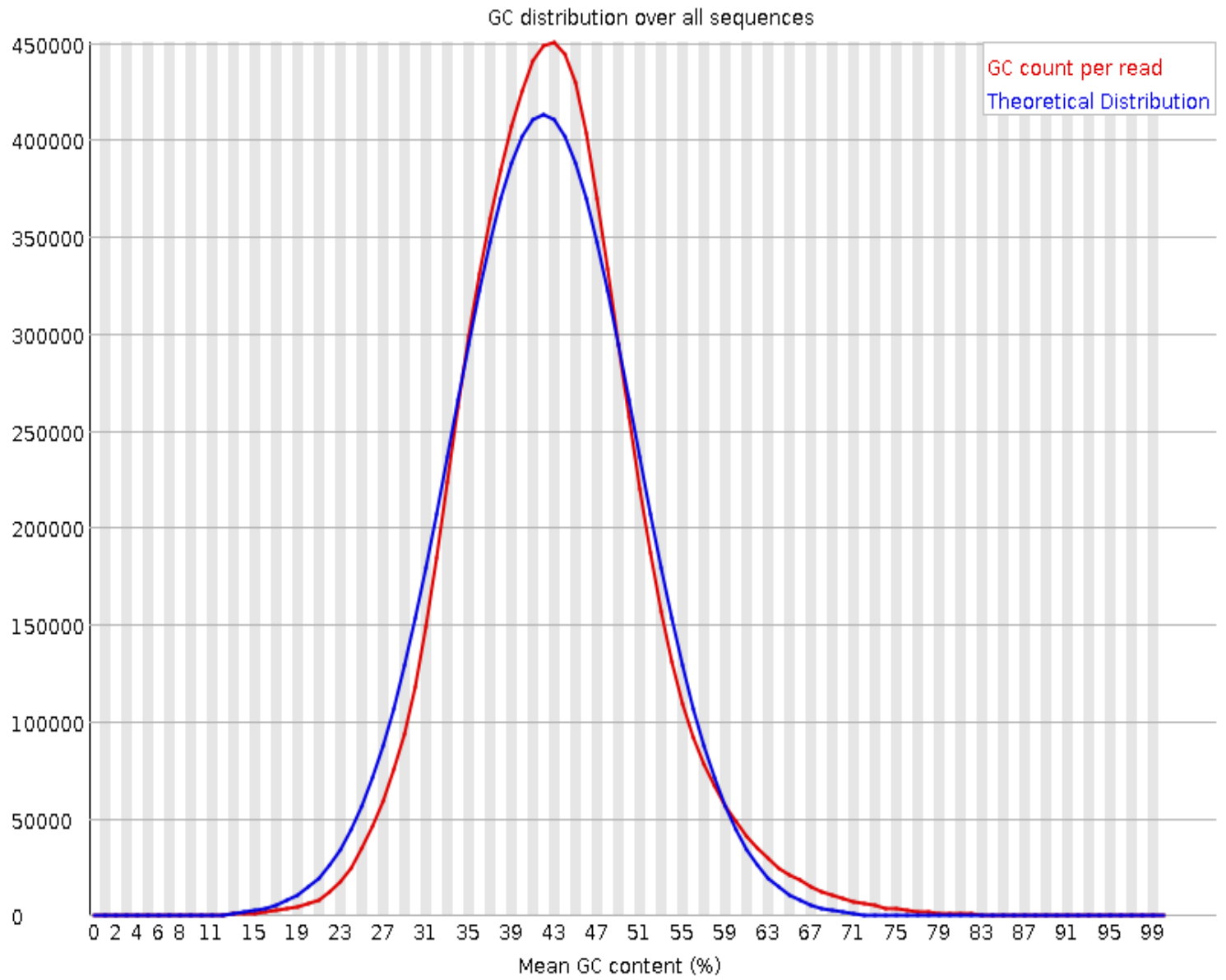


## Per base sequence content

Sequence content across all bases

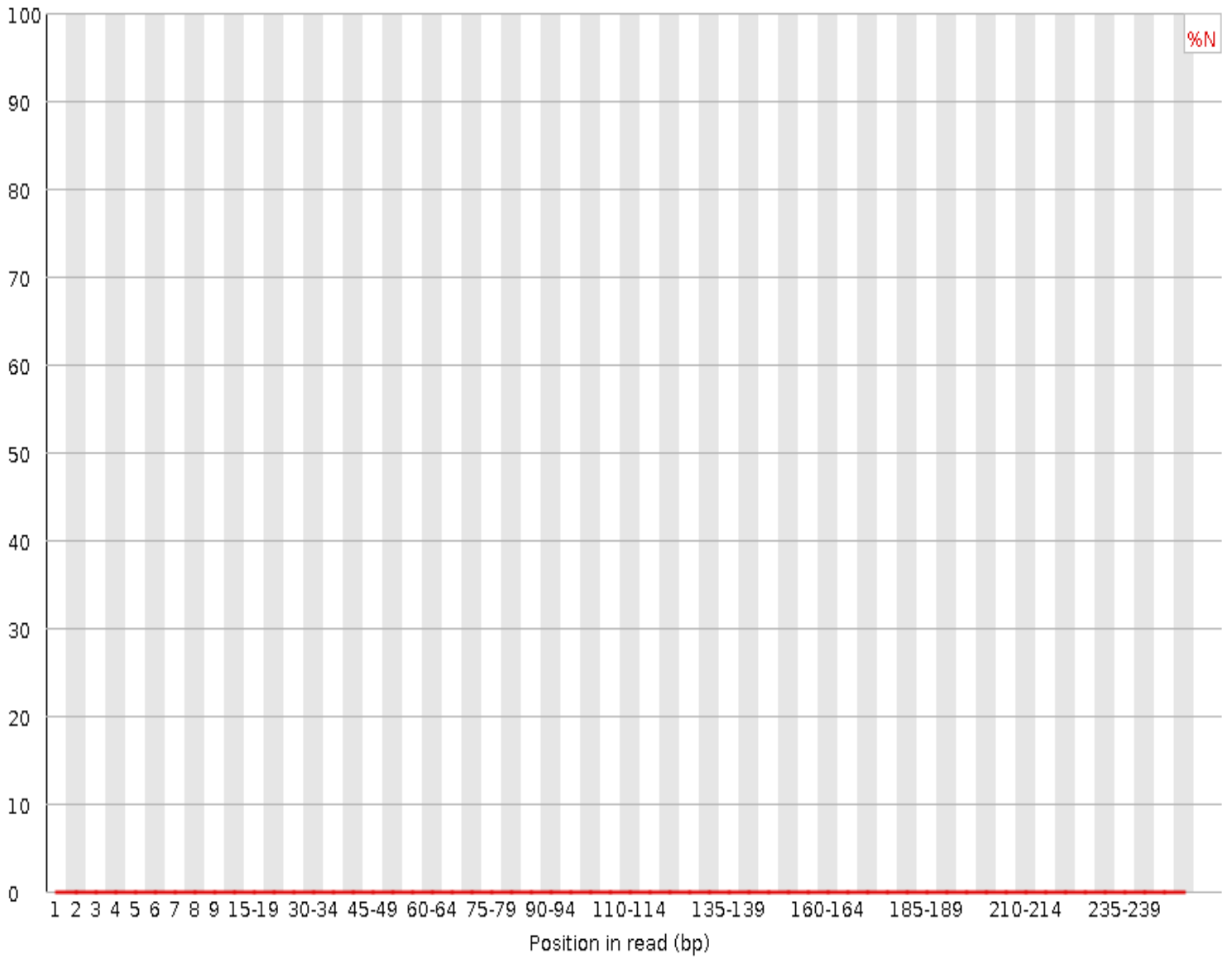


 **Per sequence GC content**



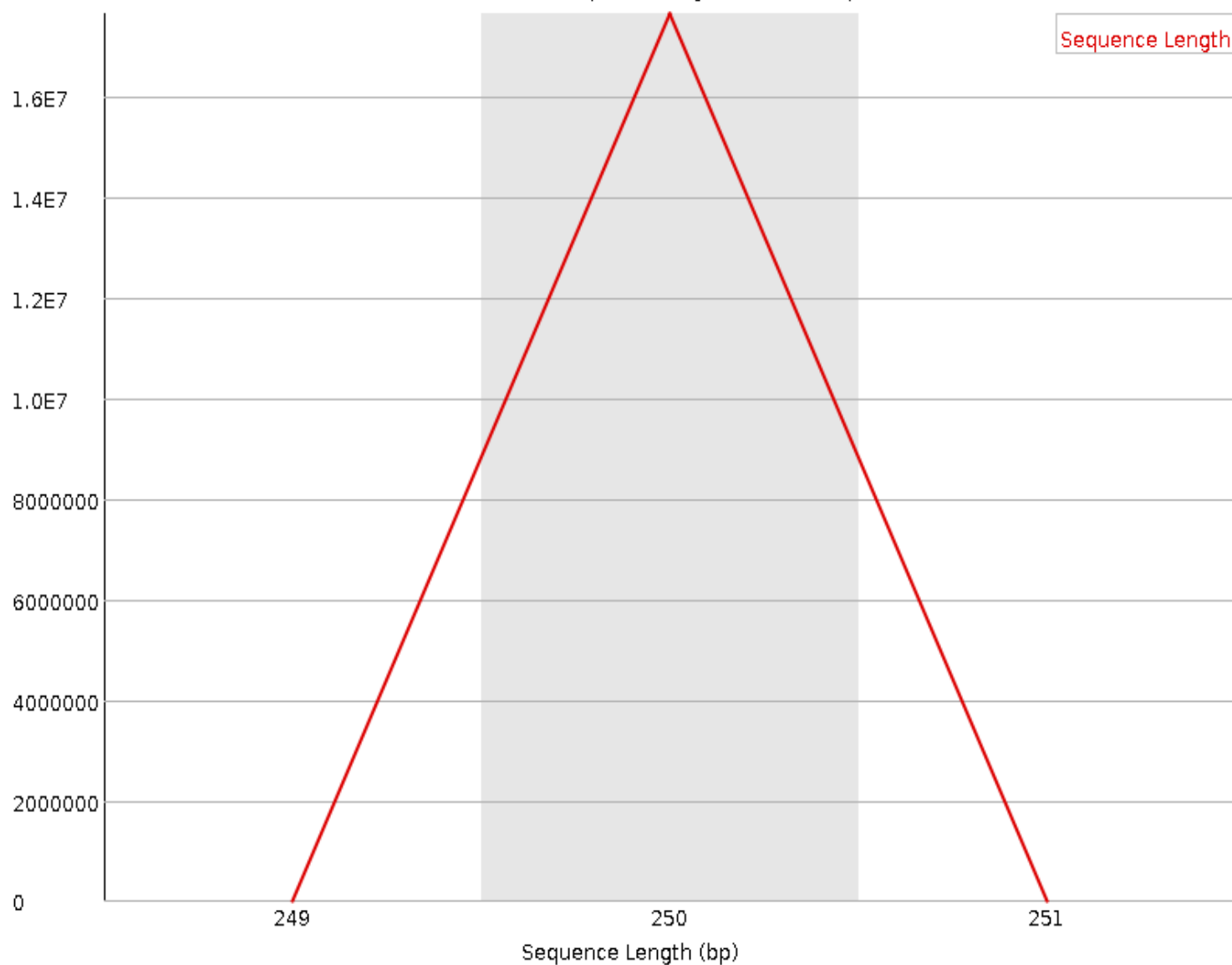
 **Per base N content**

N content across all bases



 **Sequence Length Distribution**

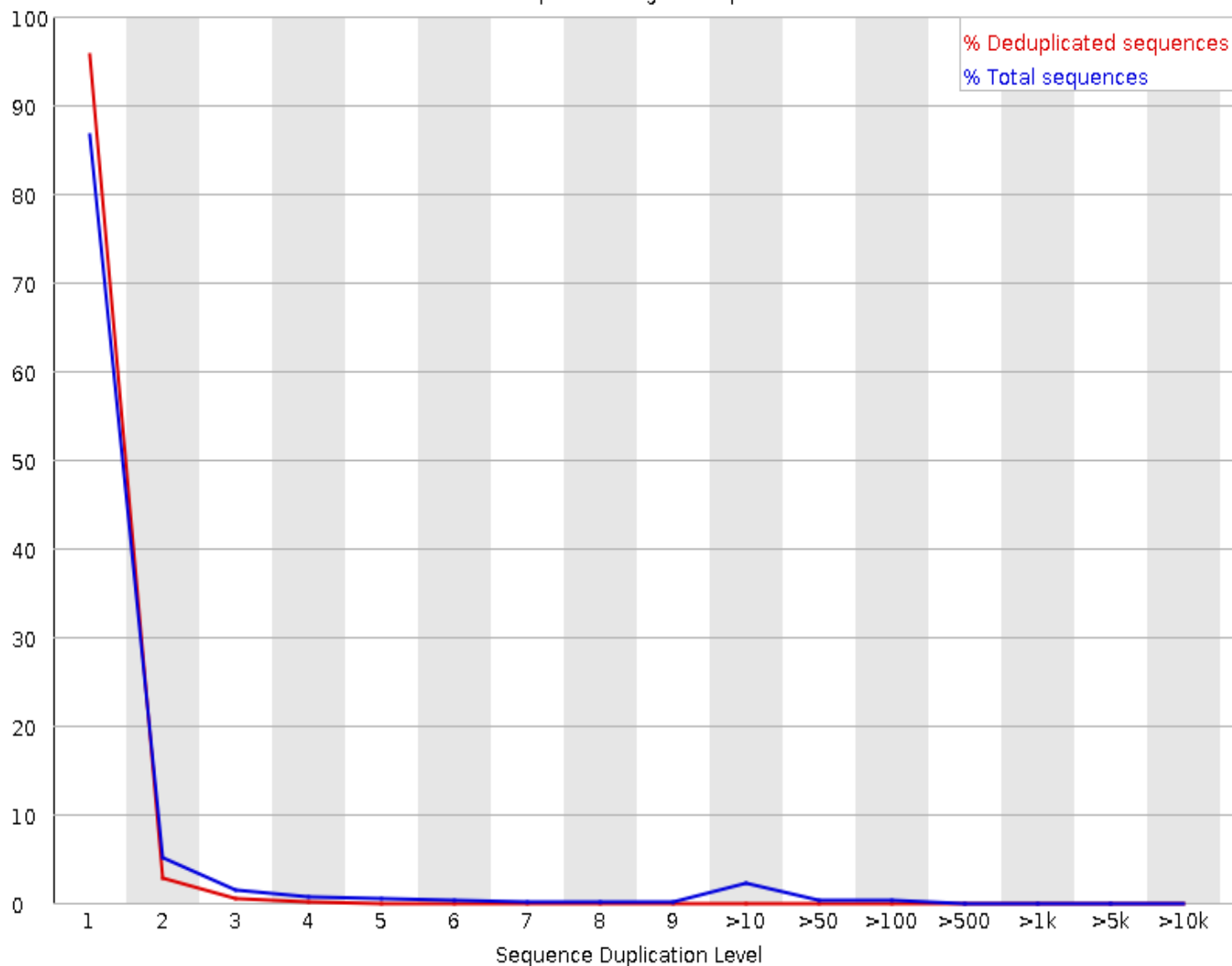
Distribution of sequence lengths over all sequences



## Sequence Duplication Levels



Percent of seqs remaining if deduplicated 90.64%

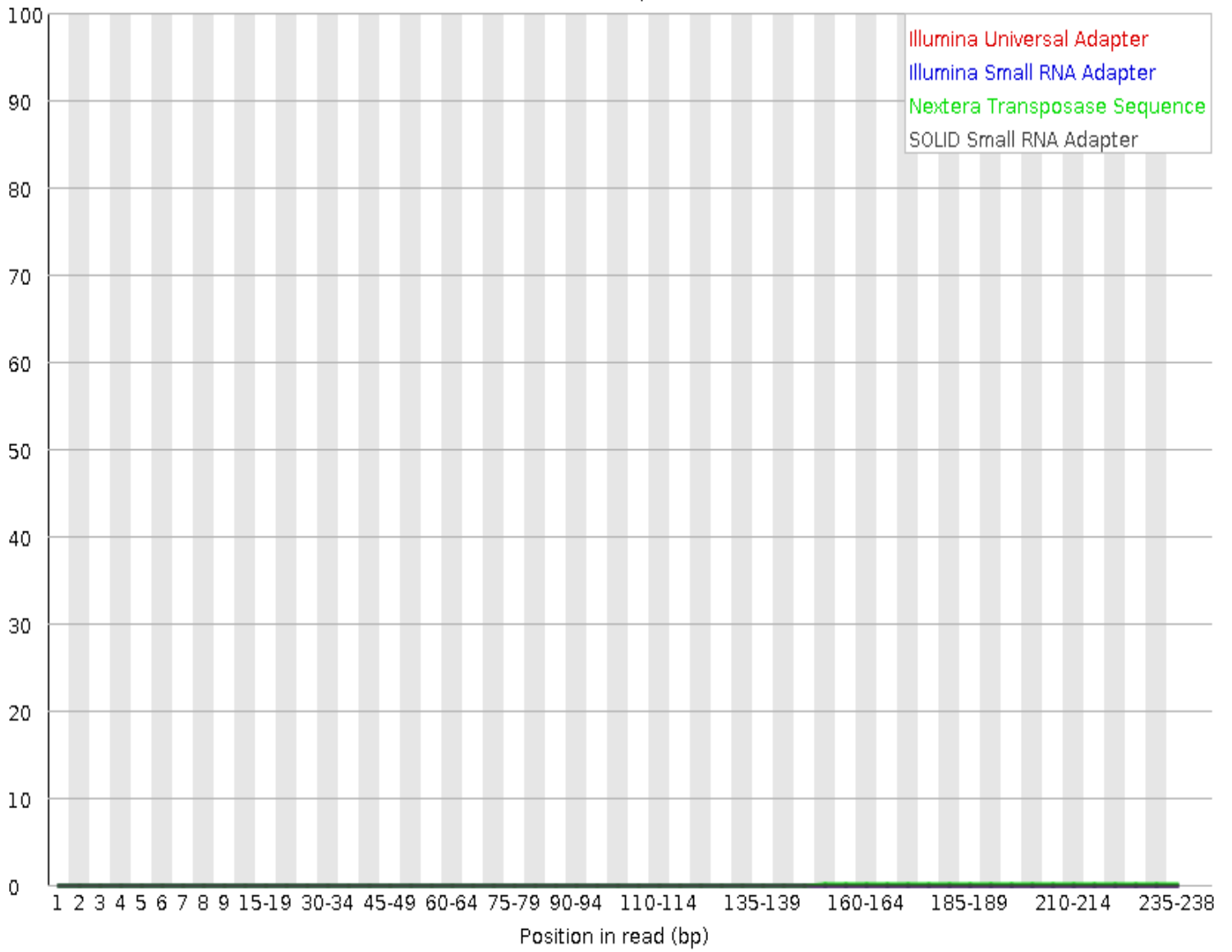


 **Overrepresented sequences**

No overrepresented sequences

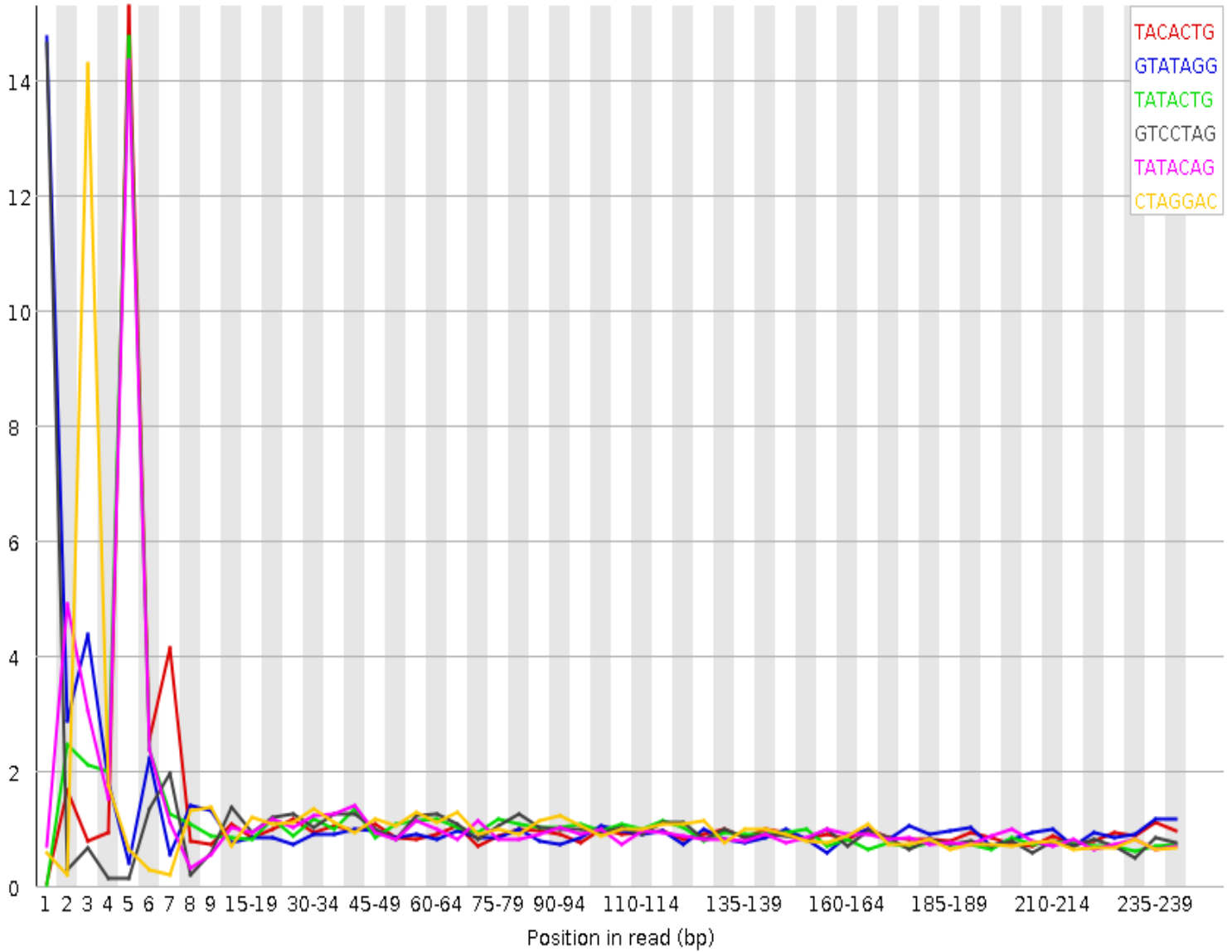
 **Adapter Content**

% Adapter



## Kmer Content

Log2 Obs/Exp



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
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TACTACTG	32275	0.0	15.272464	5
GTATAGG	14720	0.0	14.753753	1
TATACTG	46250	0.0	14.746674	5
GTCCTAG	16070	0.0	14.653174	1
TATACAG	37490	0.0	14.352156	5
CTAGGAC	16465	0.0	14.301317	3
GTATAGA	24700	0.0	14.127308	1
CCTAGAC	18120	0.0	14.0724125	3
CTATACT	23185	0.0	13.945457	4
CTGTCTC	100370	0.0	13.753358	240-244
GTATATA	40835	0.0	13.654441	1

GTCTTAG	26445	0.0	13.564197	1
GTATAAG	18105	0.0	13.410497	1
GTCCTAA	15750	0.0	13.32411	1
CCTATAC	16445	0.0	13.131667	3
GGACCGT	8000	0.0	13.116032	6
CTAGACT	22785	0.0	13.065763	4
GTGTAAG	28040	0.0	13.053699	1
TACACAG	38245	0.0	13.047961	5
GTCTATA	28835	0.0	12.905362	1

Produced by [FastQC](#) (version 0.11.3)